# **RECEIVED**

JUN 2 4 2003

TECH CENTER 1600/2900



1600

#### RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/776,705B

DATE: 05/19/20 3 TIME: 10:34:

Input Set : A:\1010 SEQ LISTING.TXT

Output Set: N:\CRF4\06192003\1776705B.raw

```
4 d110 - APPLICANT: Karl GUEGLER et al.
 6 < 120 < 710 Le 68 invention: isolated human transporter proteins,
         HE LED' ACTO MOLECULE, ENCOCING HUMAN TRANSPORTER FROTEINS,
         AND USER THEFROR
10 -1140
         FILE REFERENCE: CLOOLS TO
13 - 140 CUREBUT APPLICATION NUMBER: 09/17/,705E
 [3 | 141 | COMPERN FILING DATE: 1001-02-06
The -15 comments of PRICATION NUMBER: 00/851,830
16 - 101 - FRICH FILING DATE: , 000-12-08
M + 160 - NUMBER OF SECTION OF: 38
100 \times 170 \times \text{SOFTWAFE: FastSEQ} \pm 11 \text{ Windows Version 4.0}
                                                             ENTERED
  off one think i
33 - 211 - LENGTH: 182.
14 - 202 - TYPE: DUA
25 + 213 - OFGANISM: Home Sagiers
27 <4000 SEQUENCE: 1
. E cuattocasa caagtoagga aageotgoad apgastggat aaataattaa gaadagagtg 60
19 ttotqaacat caacacaaag tggaagaaco ttaagotgaa ggtacagtat attatttaca 110
30 cugaaggggo tigigistgg acaagaaago goigacagoi caaatggato ocatggaaci 190
31 gagaaatgto sacatogaso cagatgatga gagcagcagt ggagaaagtg otocagatag 140
30 ctacatcagg ataggawatt cagasasaggo agcaatgago agtcaattig ctaatgaaga 300
33 cactgaaagt cagaaattoo tgacaaatgg atttttgggg aasaagaago tggcagatta 300
34 tgetgatgaa esecatedeg gaadcactte etttggaatg tetteattta acetgagtaa 420
35 tgccatcaig ggcagiggga toctgggett gicciatgcc atggcciaca caggggical 480
56 activitata atcatocide itgetgigge satattates eigitaticas iteacettit 546
27 attawawaca gocasgoasg gagagtettt gatttatgas aaattaggag aawaggestt 600
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gheasgetae etenthatea thaaatatga achabetgaa ghaateagag canteatggg 770 achteaagaa aatachgag aatggeest caatggeaac taccheatea tathitgighe 780 41 togitgaach atheitreac thicogeteet taaaaaathia gghtatetig genataceag 640 41 togaithee ethacetgaa tggtgithit tghtagtgig ghgathaca agaaatheea 900 41 aataceetge eetetaceeg thitiggatea bagtgitigg aanetgleat teaacaacac 900 42 gittecaatg eatgtgitaa tghtaceesa caachetgag aghtetgatg tgaachteat 1010 40 teatgacagi gagtagaat aagaageea aagageteet 1010 teatgacagi gagtagaat aagaageea tagaageea tagbgatgaa eeaaatacht 1140

36 tygatggcog ggaaaaattg gagottttgt ttocattaca atgcagaaca ttggagcaat 660

47 totattoads tocoggacy, octational tochatosta gtatttgott tigtatgota 1700 48 chotgaggto stoccatch adaptignet taaagatogg tocoggagaa anatigdaads 1200 49 gitgtoada: atticoatca ogggaatgot tigtoatgtas otgottgoog contetting 1800 50 tracerans tigtoatgas of stockatch of the context o

50 timestance iteratggan auginguaga ngaantachi batyobiada gbaaagtgia 1190 Li tabattagan atbootbit i teatyging betynbant betydiggaag taababaada 1440 Li tytgeboani gbootbit batagtig atbaytgatb abaytgitat itebbaaaag 1100

5% accettedge tygutaegae atttoctqat tycagetyty ettattycae ttaataatyt  $1\% \psi$  54 tetyyteate ettytyeesaa etataasata estetteyya ttestagygy ettettetye 10,0

RAW SEQUENCE LISTING DATE: 00/19/2003
HATENT APPLICATION: US/09/776,705B TIME: 10:34:20

Input Set : A:\1010 SEQ LISTING.TXT Output Set: N:\CRF4\06192003\1776705B.raw

55 cactatgetg attittatic ticcagragt tilttatett aaactigtra agaaaquaac 1680 56 tittaggica occasaaagg foggggetti aattileett giggitggaa tattetoat 1740 57 gattgjaags atggeactea tialaaltuu etggattial galeetenaa atteesaugea 1800 58 tractaácar aaggaaaaat ac 60 <210> SEQ ID NO: 2 61 <.:11> LENGTH: 547 62 - 12> TYFE: PHT 63 <.:13> ORGANIGM: domo Sapiens 65 < 1002 SEQUENCE: 2 65 Met Asp Pro Met Glu Leu Arg Ash Val Ash Ile Glu Pro Asp Asp Glu 6 ' . 10 6: For Ser Ser 3ly 3lu Ser Ala Pro Asp Ser Tyr fle Arg fle Gly Asn .) [ 6) 20 7) Ser Glu Lys Ale Ala Met Ser Ser Eln Phe Ala Asn Glu Asp Phr Glu 4() 7. Sor Gla Lys Phé Lei Thr Asa Gly Phe Leu Gly Lys Lys Leu Ala 55 60 7: Alsp Tyr Ala Asp Glu His His Pro Biy Thr Thr Ser Phe Gly Met Ser 7.0 75 76 Ser Phe Ash Leu Ser Ash Ala Ile Met Gly Ser Gly Ile Leu Gly Lou 3.5 90 95 7: Sor Tyr Ala Met Ala Tyr Thr Sly Mal He Leu Phe He He He Leu 7.0 100 100 100fil Dau Ala Val Ala Ile Leu Ser Leu Tyr Ser Val His Leu Leu Leu Lys 115 12 1.5 â.: Thr Ala Lys Glo Gly Gly Ser Leu Ilo Tyr Glu Lys L∞u Gly Glu Lys 55 130 135 140 54 Ala Phe Gly Trp Pro Gly Lys Ile Gly Ala Phe Val Ser Ile Thr Met 85 145 150 155 160 66 Glr. Ash Ile Gly Ala Met Ser Ser Tyr Leu Phe Ile Ile Lys Tyr Glu 165 176 175  $\frac{1}{2}I$ is Leu Pro Glu Val Ile Arg Ala Phe Met Gly Let Glu Glu Ash Thr Gly 8 + 180 181 190 90 Glu Trp Tyr Leu Ash Gly Ash Tyr Lou Ile Ile Phe Val Ser Val G.y 90 195 200 205 9. The The Deu Pro Dea Sor Dea Deu Lys Asr. Dea Gly Tyr Deu Gly Tyr 215 94 Thr Ser Gly Phe Ser Leu Thr Cys Met Val Phe Phe Val Ser Val Val 233 230 Foo Ile Tyr Lys Lys Phe Gln Ile Pro Cys Pro Leu Pro Val Leu Asp His 250 245 98 Ser Val Gly Ash Leu Ser Phe Ash Ash Thr Leu Pro Met His Val Val 99 265 270 100 Met Leu Fro Asn Asn Ser Glu Ser Ser Asp Val Asn The Met Met Asp 101 275 280 7.85 102 Tyr Thr His Arg Asm Pro Ala Gly Leu Asp Glu Asm Glm Ala Lys Gly 103 290 295 300 104 Fer Leu Eis Asp Ser Gly Val Glu Tyr Glu Ala His Ser Asp Asp Lys 105 ...05 310 315

DATE: 06/19/2003 PATENT APPLICATION: US/09/776,705B TIME: 10:34:20

Input Set : A:\1010 SEQ LISTING.TXT Output Set: N:\CRF4\06192003\1776705B.raw

```
106 Cys Giu Fro Lys Tyr Fhe Vai Fhe Asn Ser Arg Thr Ala Tyr Ala 11e
                    321
                                        330
108 Pro lle Leu Val Fhe Ala Pho Val Cys His Fre Glu Val Leu Pro Ile
                345
1()9
                                    345
110 Tyr Ser Glu Leu Lys Asa Arg Ser Arg Arg Lys Met Gln Thr Val Ser
            355
                                360
112 Asm I'e Ser lie Thr Gly Met leu Val Met Tyr Leu Leu Ala Ala Leu
      370
                            375
                                                380
114 Pag Sly Tyr Lau Thr Phe Tyr Gly Glu Val Glu Asp Glu Lau Leu His
                        390
                                            395
116 A.a Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg
                    405
                                        410
119 Lou Ala Val Lou Val Ala Val Thr Gln Thr Val Pro Ile Val Lou Phe
113
                420
                                    425
12) Fro Ile Arg Thr Ser Val 116 Thr Leu Leu Phe Pro Lys Arg Pro Phe
           435
                                440
1.2 Der Tro Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn
1. 3 450
                            455
                                                460
1... Ash Val Leu Val IIe Leu Val Pro Thr IIe Lys Tyr IIe Phe Gly Phe
                       470
                                            475
I.o sie 6ly Ala Ser Ser Ala Thr Met Leu IIe Phe IIe Lon Pro Ala Vai
1...
               485
                                        490
11% Pric Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys
1.9 500
                                    505
1: \ensuremath{^{\circ}} Val Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met 1le Gly
                               520
1:. Cor Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser
                           535
13 \ 530
                                                540
134 Lys His His
1 - 5 - 5 1 5
13- -0:10 - SEQ ID NO: 3
139 + 111 + LENGTH: 32373
140 - 1112 - TYPE: DNA
141 -113 - ORGANISM: Homo Sapiens
14: 4400 / SEQUENCE: 3
144 ayot agcaa tanggatcaa gaggtocaat acotgattaa taaaasttto aggagtaaac 69
14	au awag_{1}ggaag aawtagtitt tittaaatagt agaastittit titattiitag aawatgigti 1.50
140 thotatagaa gawagacaag obtititgati gggbogtotig catgotyaqt atqatqaati 140
14" thaasagoga otbacatota gtoacgtogt gatgaaagga taaggataaa asttotgaaa 240
14% teeteagawa accategata aattatetat aaagaaataa gageeagaet cateaataga 300
140 agotagaaga gagaagttic tidaatatic tgaaggaaaa tgottotgaa totagaatto 360
150 ahacaattaa baaagtttga aggcaaasta aagaatttto caacatgaag caactcagaa 47.0
191 a:tetattta dagadatagg otdattgtgt gaaaaaagtt attdaaggda trattttage 480
150 ataatgcaaa ataaactgaa gaaagaagat agaatgccgt tcaagaaact agcagctgag 540
113 chagacteag aggittggagg aggaagesat teagaatgag aaagageata gaaaattige 660
1\% titoaaagti tiggtaatat agaattatat tioactiati atgiagtoaa atacaccact 6\%
115 trigicatting ggoataciat italiacaging ataliacing autifective third 7.00
156 ocatgittag aaacaaccta caggeaagtt atgacacttg titcacagaa caagatgaaa 760
157 arattatgat totoaaattg taaaagtatt ttattaacta aaataattag gagtgtagga 840
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PATENT APPLICATION: US/09/776,705B TIME: 1):34:20

DATE: 06/19/2003

Imput Set : A:\1010 SEQ LISTING.TXT

Cutput Set: N:\CRF4\06192003\I776705B.raw

113	gaaqqaagga	і аадаандааа	aagtatgota	atgtocttat	fitttatggg	taaccagt it	3c 0
1 3	r anaatbagta	: aaccaagtca	aaaaagittt	agtgaattat	tcagatetag	aatdddtaac	3000
]+)	l titaagtaac	: вафсtнавав	cagaaaccgt	caatagtggt	tactactada	aaqtqaga::t	10
] + .	- quiactgigt	gaagaatgag	gaaaaccttt	gtacccantt	adtomoutto	itiittiiti	1 .> )
1	l dittiadeca	-tatychigte	ttacttctat	totatothag	cttttaacst	gettet fit d	11.40
11.3	<pre>-afcttttatg</pre>	tatatacatt	taggotgoot	tatastasta	ataonttcat	ttttatteet	
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1 + ::	gadaattoto	tgccat tate	totttotgtt	ttatatataka	ctagnetes:	satt stotat	7 - 4
1+6	atinggaanga	ctatoagtgt	atatttgaac	ttqtaatict	tattititi	cattoffet	1 - 5 1
1.	taacttotta	totqtatttt	tottttttta	atotottnat	actataarre	paginaritic	1.11
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1	gastotastis	titiutittt	tttaaqaatt	oostastita	artetitte	- caacacactin	
1	itotoctitt	atationitit	ataatqtttt	tattotatas	aaattattit	offattttda	le ii
171	argtittett	toaaaatgto	tttotittta	ttaatttaat	- ataasaatic	- ottt tsalatt	1
1	grittigttat	tigtagitos	ttagatgtga	atititatoat	trictit at acc	fact renact	1 313
173	utugotagtig	agittecatg	tatattatat	atattttata	atti uaddat	atas attit	i an
1/4	stcaagtgtg	agitgootti	caaaaaaaata	ctgouatge	act gagging	oragination to	17.0m
175	brat jtiggt a	gittergitt	gtcadaddaa	tagdadatht	tatasettit	- mgaggealto	Tigal Ha
176	itatyttägt	itototycto	aagatttoot	tatosaa+gg	of attricada	tatostadec	1 a - n
177	acacttttca	agaatqutag	tatttataat	aatacdatidd	-titoaacaata	attraatmaa	10.10
100	· chautggt i	agaasi sag	advada, Jak	atCaadLada	laradrádar	Tidaado catit	2040
170	tttchaaaaac	adaatigocag	tecaccectt	ttcactatac	aattoaddaa	- aatayguice	2000 2006
1:0	ccaaatgtta	aatga:mtct	getgagatee	aatdaattaa	addoadadda	ranging yees	1.00
191	totagatoto	tttgttgtta	aaatacattt	taatttgaca	cagat dat da	at sat not de	200
1	necagagata	aatotgaact	ttettttatt	actatictia	actitogett	geddigolga Gaddlethaaa	1.00
193	gtgcctagaa	agttacttcc	taaacttgat	cctcacctat	attacatatt	atraamratt	240
154	iggiggiati	aattotttca	totocaatta	aattaaagca	graattttct	ttotagtist	23.60
1:5	tgctagtaga	gacactggta	gattetgect	togtagacet	act ctatica	acaatttact	26.50
156	tttglettes	tttcttttaa	aacatqtatc	ccact.cacaa	atacctaaat	ttccttgaag	1590
167	actgotgoca	tgttttaaga	tttcttttt	tttccatagt	gactagtasa	acctroccatt	1630
188	ttcattatac	ataggcacto	tataaatatc	toctaattta	graattatta	at a at t t cot	2700
189	ttottotott	ccattlette	ctttcttqta	ttgggtaaag	gaacat*tca	geauttestt	2760
130	atgtaaagtt	ttcaggagtt	tettteette	ctccctttta	cadagagcat	acasastata	28.00
191	gatgattcat	attcacttat	ttcatttaaa	taaaattata	atbatotato	ttatattata	1890
192	tttgcagaac	agagtgttct	gaacatcaac	acaaaatoaa	adaacettaa	actasaarts	2930
1:13	cagtatatta	tttacactga	aggggettet	atataaacaa	gaaagcgctg	acadeteaaa	3000
194	tggatcccat	ggaactgaga	aatqtcaaca	togaaccada	tgatgagagg	addagtedaa	3000
195	aaagt.gct.cc	agatagetae	atogggatag	qaaattcaga	aaaddcadca	atdadcaddt	31.50
196	atggggttaa	aaattactat	gttccataga	aaaataagac	addatatada	catagaaaaa	3190
197	agggtettga	tgggaagaac	tqqatttatt	acaddtaast	ttataataac	aatmatatta	3310
198	atgotagoad	atcaattccc	taatootaaa	atacagtgat	aatotoaato	tetttetes	2300
199	ctgatttaga	attgaggtta	caatgtottt	gtotocatta	ataatatat	ataattttas	2269
200	ttattttäda	ctattgetee	tottatofff	ctcacattcc	totttrasta	ttaatsasaa	0.000 3.1.00
201	tootgattta	tgtagggatt	cttttatata	tasaantato	ototocyaacy.	aratasatasa	24.0
0.0	aadtactato	gcotcaccot	ccasatatat	docatatace	carcetatto	guidaducad satttatata	390U 3010
.103	ctimattica	gataattata	totgaatgto	tactocacat	oughouguld ototactors	aguittetta.	2049
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. (:5	todotodaaa	acctgetest	cototagtaa	torpostort	antmaaaata		30 HU
<u> </u>	tgtagsaach	cactcaaaag	cocctagedu	taaaatttko	ogegadati.	autyttaidä	27.3
	2	g	- Joseph Grand Grand	cadabillyd	colalatayo	caabygtdag	57:0

DATE: 06/19/2003 PATENT APPLICATION: US/09/776,705B TIME: 10:34:20

Input Set : A:\1010 SEQ LISTING.TXT

Output Det: N:\CRF4\06192003\I776705B.raw

```
207 teatatecag tiggittgae ettattaatg etteaaatac aeetaettit etgiaeecai 🤭 10
 nn8 totactgigg fottacgita ggostalatt adalgigaga cagggagaga gccetgatit
 . eta electrocity, elementatic get terret yequagecet etabactect geaagageaa -960
 .10 totottseaa tigeasatig aat aaitte cateettaja taaageeett eigearetet 4\geq\!0
 . II obaatagoda (aagagaaag tagsttodad aquetgetgg geangtaagg tecittytga 🕒 )
  12 tetgitering accordanced conjunctiff tittinged to consist givening to 4.10
 .13 geottoacte attorjetee aastgeetgg äatcagtese etg temede ificielgig 4. )
  A tigacacete icasestica agasteaget caacateagg tot clatge ageotitice \{+\}
  In anattactet reterrocat grayangiga eigeneeted tientgrade stotechtet 4 \odot 1
  ^{\circ}6 goaqatqtta attacqeeae fastacaggt taatqqeete tqt^{\circ}qteeca ceaectgeea (\cdot,\cdot)
. \mathbb{N}^T satisfietog todatagtga ofgradaata gittättigat aagreaatig atticosaca \mathbb{N}(\mathbb{N})
\pm 1.13 adatystata icaaastyta kaiqattiaa gaigkicaga aggkaattii igadbaaato 400.0
...) taggogtgaa atagagaata (tyngotoaa abaaagaont oto:tthtat ntabiacaco 4000
...) caggaamate catcaquaga aactaccytt ettecttema gtaletbagt qeaatglast 40.0
\dots ) thaggerigt eggressaga aggreeactya gatgtsaatt atalicattit otaaachagg \oplus \cdots
...! tgaccettga aşalacarta oggtgötaga agacaşggöt ttgdagtetg bagagtigtt 4 40
.. 3 gootgabilts agamangerg ittigtborbt tigagettba atgrassatg sassatgers 4/...
... aabcaacago tydriftcaa (gatgagatg gytysccaya atalagatga Battcaitac 4000
LIB tittitatta ottotootto aetgeattae eetgagtaaa tigattoaaa ootgaggatg 4920
... i titicigasag geatgeacae asatatgage tetgecoagg tigacagagt taaaggggae 49-1
 . M. adoctichau yuun missas ayliyesseed dadolgaams (dawaaqood qagtagsaag mys)
{\mathbb R}^{2n} agreety-eaty office to a gottouty our argustness sacractical agreements of {\mathbb R}^{2n}
.u. otottatoto orgooffaaa hataggabat oatottgoag titttaäaat bagtotsaag "]eo
The agatogogite tatefatgtg toggistegat togadesetta aatotaaatt sitgagaaat filo
... I toaabataan goafffatti gogatbatta taboogtgoo tebaatabat googgoodig 5/80
73.6 gtateaasas atttaaesta stygygaest ttetesteta tettataesa tettygesty 5 \pm 4 \%
.33 ttaaatgact acaactcate teatgecaaa ataagaabat geaaatgeet caaagaaaga 5400
134 aaatotgitt sotticaaat titoaattit aaaaaotact aiggaataca mattitagit 5400
{\mathbb R}^{n} taltqattam matamagatt ocagagitta mattetaggi ggcaetting intitaragi {\mathbb R}^{n} , {\mathbb R}^{n}
. In obtoaggood attitisagest toattitiate offgtoatoto agreeocase tytigaacatt 5(\pm a)
237 átgtaccagt citicacatag caggitacatt aattacagad cattaatgia aaccacsaaa (640
2% gagtiggtogir cagtigggtigg gyggtigaatig gaaatiggaaa gaggbaacsa ctgagggcat 5700.
179 tgtgotttot gtgagaaata tggggagaag gotaggaaat gttottaact tgtgtactoa 5760
040 gagetattta tgocttgagt tetagaaaag cacamacaac tttgtggttt cytgtgctgt 5900
142 tectatotac atotoatact gittietatt eteawaaagt aaccotgica footoirtee 5670
. AL tetecagatt attitoagga tiagettetg tiataaaaaa tageitgiae agateleeta 1940
\pm 43 caataastat tittetatiiti ahittetaagg tittätittätt hattiattya gadagadaga \psi \theta (\phi)
. 44 gittemetet tytygecemt getygmytye mmtygtyemm tetegygetem etycmmete 6060
245 tgcctcccag gttcaagcga ticthotget teagesteet gagtagetyg pattacagge (720)
146 gootgobabb ababtegget aucthtitgt attitetagta (agangaagt ticabbatgt 6180
. 47 tggodagget ggtettgaad toetgadeto aagttateda bedahetdag estdecaaag e. 40
UNA tgetgggatt acaggegtga gecaetgtge etggeeteta ggattatatt astagaacaa n3e8.
1.49 tottomatta tittatetit ettiatetit ettitemigt aggmantgie etmmätti 6.560
[30] daaacootsa atttgaasgo asttitaaaa toatacatag togagoatit tatataaaaa +4.00
Ptl caactalaaa gtolgtgaca tittigdagta caaaaatgda atggbagbag eliggeettat 6480
If I tauttgaged tetriggaaat griggetiggte etaggroegt agestsaag geostggett. \mathfrak{C}4\mathfrak{o}
. Do gtaactgcag gagotgacca goacagotet ataaccaagt tgtacateft chageotgtg from
U(4 tocaagaasa coagastoso asegetetgt ggatagtgas atettaaagt titettteed 600)
:ff tecesasetet titigecagit eatigaatig eittaataat tieettagit teaticatia 6/10
```

#### VERIFICATION SUMMARY

VERIFICATION SUMMARYDATE: 06/19/2003FATENT AFFLICATION: US/09/776,705BTIME: 10:34:21

Imput Set : A:\1010 SEQ LISTING.TXT

Output Set: N:\CRF4\06192003\I776705B.raw

JUN 2 4 2003



1600

#### RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/895,041C

DATE: 05/19/2003 TIME: .0::2:23

Input Set : A:\AP09895041JUN1003.txt

Output Set: N:\CRF4\06192003\I895041C.raw

```
3 4110% APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY
        SEU-PEI, WU
 6 TIZE OF INVENTION: A NOVEL PHENYLALANINE AMINOTRANSPERASE AND ITS USE
   1120 FILE PREFPRICE: US-2812-CHN
1 +14 + CHRRENT AFFILICATION NUMBER: US (9/895,041C
11 \times 14 \mapsto \text{CPFEENT} FILLING DATE: .0001-06-09
1 - 10 NUMBER OF SEP II NOS: 31
1' -150 SCHTWAFE: FatentIn version 3.7
                                                           ENTERED
17 - 210 - SEC II NO: 1
18 - 311 LENGTH: 1199
10 - 1111 TYPE: INA
```

#### 3. .10: dipanidii: Astherichia (c): .. -400 SHQUENCH: 1 23 augitthasa asuntgungo obangolggo garbogatto thacgolhat ggagogitti .5 Asaqaagand offigeaqnga caaagtgaat titaagtatog giotytabia caabgaagad 1.10 17 ggaattatto camaactyda agoogtogog gaggoggaag ogogootgaa tgogoagoot 180 19 categogett egytttaltt acceategaa gegettaact getategoca egetattgog (41)31 togotgetet tiggtgodga odatooggta otgaaacaad agogogtago aadoattoaa 390 33 acceptages octoograss attgasagts geographit tootgasags starttoog 360 35 gaatbaggeg telgggteag cyaloctace tyggaaaace abgeageaat attogebygg 420 37 getugatteg aagtjagtad ttacccetgg tatgacgaag egactaaegg egtgegettt 460 39 aatgaootyt tygogaogot gaaaacatta betgoobgoa gtattytytt gotycatoba -540 41 tyttgocada adicaacgyg typogateto actaatgato aytgygatgo gytyattyaa -43 atteteaaag coogegayet tatteeatte etegatattg cetateaagg atteggtgee 45 ggtatggsag aggatgeeta egetattege gecattgeea gegetggatt accegetetg 720 47 gigageasit egittetegaa aattitotee etttaeggeg agegegiogg eggaettiot -49 gltangtyng aagatgeega ageegetyge egegtaetgg ggeaattgaa agewaeagth $\mathcal{G}_{\mathcal{A}_{i}}(j)$ 51 egoogbaadt autobagede googaatitt getgogbagg tygtggotge agtgotgaat 900 is gaagaggest thesagerag etggetggeg gaagtagaag agatgegtae tegesattetg 96.0 55 qcaatgogto aggaattogt gaaggtatta agcacagaga tgocagaacg caatttogat 1000 57 tatobgotta accaquyoyg cabgitbagt tataboggit taagigoogo toaggifqab 168659 ogaetaegig aagaatitig tigtetateti ategodagog giogoatgig tigtegooggg 1140 61 thasatabay casasiglada adgitgiqda aaggogittig oligbggtgal glaatgito 1199 64 + 110 + SEQ ID NO: f65 - 11 - LENGTH: 1199

- 66 -Dil. TYPE: DNA
- 67 (11: ORGANISM: Escherichia coli
- 69 (400) SEQUENCE: 1
- 70 atgittoaaa aagtigaego otaogotggo gacccgatto ttaogottai ggagcgitti  $-e^{i\phi}$ %) assistagado otogoagoga casagtigast ttaagtistog gtötgtabta caabgaagad 1. 0 74 gynastatto cacaactyca agoogtygog gaggoggaag ogogootgaa tgogoagoot -180 76 citygogott ogotttattt acogatygaa gggottaact gotatogoca tgocattgog 2.0 To constgetyt ttgytgsgga csatssggta stgaaasaas agsgsgtags aassattsaa 300

DATE: 06/19/2003 PATENT APPLICATION: US/09/895,041C TIME: 10:32:23

Input Set.: A:\AP09895041JUN1003.txt Output Set: N:\CRF4\06192003\I895041C.raw

(V) apporting to get toggang attacks at a many	
NO accettrary geteegggge attgaaagtg ggegeogatt teetgaaacg etactteeeg 32 gaarra:: g tetgggteag egateetace tyggaaaace acgtagcaat attegeeggg	360
4 get main g aagtyagtag tracecetigg tatgacgaag egactaacgg egtgegettt	420
in matine in the propagate conducting tangangang egantaneng egingegetit	480
)	540
: itt carring corregaget tattecatte etegatatte ectateaagg attiggtgee	600
in 13th grand againteent citedatated detacted aggregate acceptete	660
[14] (Eg.) (E.) (1. Dg.) (Stogaa aattitotoo otttaoggog agogogtogg oggactitot	72)
" unit i at it is abundanced aggregation organization in the second control of the secon	78:)
figuriting in granitycega ageogetyge egegtaetyg ggeaattgaa ageaacagtt	84.)
90 - To Mora the activisações geograficate gotgegnagg tygtggetge agtgetgaat	90)
3 ia iaurist turaageeag etggetggeg gaagtagaag ägatgegtae tegeattetg ii i2miturise ärriatsggt gaaggtatta ageacagaga tgecagaacg caatttegat	950
in the same aggregation and aggregation and the same aggregation aggregation and the same aggregation and the same aggregation and the same aggregation a	1620
The the threaten services to the table of the same and th	10:0
I'm organization of a managed and a state of a suppose of the state of	11:0
1:7 Theathogy Westgtaca acgtgtggca aaggegttig etgeggtgat gtaatgete 111 22:5 (Fig. II in: )	1149
1! - All - Famorn: [4	
10 21 TYPE: DUA	
114 - 212 - FWANSW: Escherichia coli	
13: +40 - FEQUENCE: 3	
107 mars ning and adaged tally	
1.00 + 210 + 2Eq. 15. (3): 4	. 4
1_1 + 111 + LEEGTB: .:0	
1.0 + 21. TYPE: 01W	
1.3 - 11 / OFCANISM: Escherichia coli	
1.5 · 400 · SEQUENCE: 4	
1.6 spasgagere tegageatta	20
129 - 210 - SFO ID NO: 5	2. U
170 + 111 + LENGTH: 10	
191 - 211 TYPE: MWA	
182 - 213 - OFGANISM: Escherichia coli	
134 + 400 + Seguench: 5	
13% ggotogtata argogtggaa	20
- 178 - 210 - SEQ ID NO: 6	2. 0
139 - 111 - LENGTH: 18	
1401. MITTER: PMA	
141 - 311 - OF JANISM: Escherichia coli	
145 400 SEQUENCE: 6	
144 godattgogo ogotgotg	13
147 - 710 - 3EQ ID No: 7	• •
14% + 211 + LENGTH: 14	
149 - HIC - TYPE: LINA	
150 - 110 - 05GANISM: Escherichia coli	
15.1 + 400 + SEQUENCE: 7	
155 recomment group	14
196 - 210 - 250 ID no: 8	
157 + H11 + LEDGTH: , 4	
15 y + 17 + TYTE: ! NA	
159 - 13 - GROANISM: Escherichia coli	

PATE: 06/19/2003 FATENT APPLICATION: US/09/895,041C TIME: 10:22:23

Input Set : A:\AP09895041JUN1003.txt Cutput Set: N:\CRF4\06192003\1895041C.raw

```
161 <40 P SEQUENCE: 9
   162 accestga o trattaccaa coto
                                                                                                                                          24
   ..5 -220 SEG II NG: 9
  146 - 1111 IFNGTH: 1199
   INT STILL TYPE: ENA
  1+8 -112: CF ANISM: Escherichia coli
  . TO -4000 SEQUENCE: 3
   []] afgittessa asgituaego etaegetige gaccegatte tiaegetiat egagegitti.
  170 waaaaagaro ctrgoagoya caaagtyaat ttaagtatog gtotgracta caacgaagac
  1.11 spaattatio cacaactyca agoogtgyog gagyogyaag ogogootgaa tgogcagoot
                                                                                                                                        1 (0)
  ... rategogrit rgottrattt abogategaa gggottaabt getategoba teobattego
                                                                                                                                        \cap \Box
  1 8 sugetyetyt tiggtyegga edateeggta etgaaabaad agegegtage aaddatteaa
                                                                                                                                         3.11.1
  171 spectingly gottonggggo attgalaging ggogoggatt tootgalaang chaotheneg
                                                                                                                                        South
  It's quaticagging totggitting ogationists tgggaaaabb abgtagoaat attogooggg
  1/5 yetggattig aagtgagtad thaddedtgg tatgaogaag ogadtsaegg ogtgegettt
                                                                                                                                        400
 15% satgamente tegegaeget gaaaacasta ootgooogca ghattegtgtt gotgoatoca
                                                                                                                                        1.40
 189 rettinocaca abocamogig tycogatoto actaatyato agtgygatyo gytgattyaa
                                                                                                                                        (11)
  191 attotommag congregated tattocasto otogatating outstcmage attiggtion
                                                                                                                                        (60)
  195 gytatygaag aggammenta egetattege gecattyoba gegetggatt abcogetorg
                                                                                                                                       7.0
 195 otgaquaati ogitotogaa aattutotoo etutaoggog agogogtogg oggaetttot
                                                                                                                                       730
 ton reformation of a language ageography of control of the control
                                                                                                                                       840
 1.9 egoogbaact aeroeagedo geogaatitti ggigogbagg iggiigqcige ayiig iijaat
                                                                                                                                       GÓÒ
 101 gabgaggest tgaaagebag etggetggeg gaagtagaag agatgegtab tegbattetg
                                                                                                                                       950
 203 gcaatgogud aggaatuggt gaaggtatta agdadagaga tgodadaadg daatttogat
                                                                                                                                      1020
 205 tatotgotta atcagogogo catottoagt tatacogott taagtocogo toagqttgac
 107 egactacqtq aagaattiqq tqtctatctc atcqccageg gtcqcatqtq trtcqccggg
                                                                                                                                     1140
 109 thaaatacag caaatgtaca acgustguca aaggogtitig otgoogtgat glaatgete
                                                                                                                                     1199
 012 -210> SEQ ID NO: 10
 213 <211 - LENGTH: 397
 214 < 212 > TYPE: PFT
 015 <213/ OFGANISM: Escherichia coli
 217 <400> SEQUENCE: 10
019 Met Phe Gln Lys Val Asp Ala Tyr Ala Gly Asp Frc Ile Leu Thr Leu
                                                                          10
335 Met Glu Arg Phe Lys Glu Asp Pro Arg Ser Asp Lys Val Asn Leu Ser
                             110
                                                                   25
317 lie Gly Leu Tyr Tyr Asn Glu Asr Gly Ile Ile Pro Gln Leu Gln Ala
                      55
                                                           4.0
031 Val Ala Glu Ala Glu Ala Arg Leu Asn Ala Gln Pro His Gly Ala Ser
                                                   55
                                                                                         60
235 Leu Tyr Leu Pro Met Glu Gly Leu Asn Cys Tyr Arg His Ala Ile Ala
236 65
                                            70
                                                                                 75
139 Ser Leu Leu Phe Gly Ala Asp His Pro Val Leu Lys Gln Gln Arg Val
340
                                    85
                                                                          90
243 Ala Thr Ile Glm Thr Leu Gly Gly Ser Gly Ala Leu Lys Val Gly Ala
                             100
                                                                  105
[47 Asp Fhe Leu Lys Arg Tyr Phe Pro Glu Ser Gly Val Trp Val Ser Asp
140 115
                                                          120
251 Pro Thr Trp Glu Asn His Ala Ala Ile Phe Ala Gly Ala Gly Phe Glu
```

DATE: 06/19/2003 PATENT APPLICATION: US/09/895,041C TIME: 10:32:23

Input Set : A:\AP09895041JUN1003.txt Output Set: N:\CRF4\06192003\I895041C.raw

```
13.0
                         135
 ,55 Val Ser Thr Tyr Fro Trp Tyr Asp Glu Ala Thr Ash Gly Val Arg Phe
 16 145
                             155
 189 Ash Asp Leu Leu Ala Thr Leu Lys Thr Leu Pro Ala Arg Ser Ile Val
. 60
                         170
. + 3 Leu Leu His Prc Cys Cys His Asn Pro Thr Gly Ala Asp Leu Thr Asn
 144 180
                      135
\mathbb{R}^{23} Asp Gln Trp Asp Ala Val I.e Glu Ilë Leu Lys Ala Arg Glu Leu Ile
 1.3 195
                     200
. Allinc Phe Leu Asp I.e Ala Tyr Oln Gly Phe Gly Ala Gly Met Glu Glu
                        215
  ^{\rm th} Aug Ala Tyr Ala Fie Arg A.a Fie Ala Ser Ala Giy Leu Pro Ala Leu
                     230
                                     .≥€£,
170 Val Ser Asn Ser The Ser Lys Tie Phe Ser Leu Tyr Gly Glu Arg Val
                 245
                                 250
Jab Gly Gly Leu Ser Val Met Cys Glu Asp Ala Glu Ala Ala Gly Arg Val
260
                    265 .270
LeV Lou Gly Gln Leu Lys Ala Thr Val Arg Arg Ash Tyr Ser Ser Pro Pro
275 280
191 Asn Phe Gly Ala Gin Val Val Ala Ala Val Leu Asn Glu Glu Ala Leu
 nah kag
                        215
                                ي زيازيا
198 Lys Ala Ser Trp Lou Ala Glu Val Glu Glu Met Arg Thr Arg Ile Leu
JB6 305 310
                         315
199 Ala Met Arg Gln Glu Leu Val Lys Val Leu Ser Thr Glu Met Pro Glu
                 325
                                  330
303 Arg Asn Phe Asp Tyr Leu Leu Asn Gln Arg Gly Met Fhe Ser Tyr Thr
304 340
                     345
36.7 Gly Leu Ser Ala Ala Gln Val Asp Arg Leu Arg Glu Glu Phe Gly Val
308 355
                    360
311 Tyr Leu Ile Aia Ser Gly Arg Met Cys Val Ala Gly Leu Asn Thr Ala
                       375
                                        380
315 Asn Val Gln Arg Val Ala Lys Ala Phe Ala Ala Val Met
316 355
                    390
319 <210> SEQ ID NO: 11
320 <011 - LENGTH: 397
301 -0012 TYPE: PRT
322 42132 ORGANISM: Escherichia coli
304 <4000 SEQUENCE: 11
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307 1 5
                                 10
300 Met Glu Arg Phe Lys Glu Asp Pro Arg Ser Asp Lys Val Asn Leu Ser
351 20
                               25
314 Tie Gly Leu Tyr Tyr Asn Glu Asp Gly Ile Ile Pno Gln Leu Gln Ala
                         4 ()
338 Val Ala Glu Ala Glu Ala Arg Leu Asn Ala Gln Pro His Gly Ala Ser
                       55
34% Leu Tyr Leu Pro Met Glu Gly Leu Asr. Cys Tyr Arg His Ala Ile Ala
343 65
                    7.0
                                    7.5
346 Pro Leu Leu Phe Gly Ala Ası His Pro Val Leu Lys Gln Gln Arg Val
```

RAW SEQUENCE LISTING DATE: 06/19/2003 PATENT APPLICATION: US/09/895,041C TIME: 10:32:23

Input Set : A:\AP09895041JUN1003.txt Output Set: N:\CRF4\06192003\1895041C.raw

347	,				85											
		Thr	Tle	min		. T				90	7. 1				95	
		Thr		100					-105	)				110		
		Phe	110					- 20					125			
71 B	Pro	Thr 130	Trp	Glu	Asn	His	Уа1 135	Ala	Ile	Phe	Ala	Gly	Ala	Gly	Phe	Glu
11.3 11.3	Val 145	Ser	Thr	"yr	Fro	Trp 150	Tyr		G.u	Ala	Th:	Asn	Gly	Val	Arg	
31 6 367	Asn	Asp	Leu	leiu	Ala 165	Thr		Lys	Thr	Let 170	Pro	Ala	Arg	Ser		
370 371	Leu	Leu	His	Pro 180			Ers	Asn	Paro 185	Thr	Gly	Ala	Asp			Asn
374 375	Asp	Gln	Trp 195		Ala	Val	lle	31u 200	Lite	L∈u	Lys	Ala		190 Glu	Leu	Ile
375 375	Pro	Phe 210	Leu	Asp	Ile	Ala	Tyr 215		Glγ	Pne	Gly	Ala 220	.205 Gly	Met	Glu	Glu
411	4.40					- 230	Ala				19 G E,	Gly				0.10
386 397	Val	Ser	Asn	Ser	Phe 245	Ser	Lys	Ile	Ph.e	Ser Žov	Leu	Tyr	Gly	Glu	Arg 255	Val
390 391	Gly	Gly	Leu	Ser 260	Val	Met	Oys	Glu	Asp 265	Ala	Glu	Ala	Ala	Gly 270	Arg	Val
394 395	Leu	Gly	Gln 275	Leu	Lys	Ala	Thr	Val 280	Arg	Arq	Asn	Tyr	Ser 285	Ser	Pro	Pino
398 399	Asn	Phe 290	Gly	Ala	Gln	Val	Val 295	Ala	Ala	Val	Leu	Asn 300	Asp	Glu	Ala	Leu
403 403	Lys 305	Ala	Ser	Trp	L∙eu	Ala 310	Glu	Val	Glu	Glu	Met 315	Arg	Thr	Arg	Ile	Leu 320
407		Met			325					330	Ser				335	Glu
410 411	Arg	Asn	Phe	Asp 340	Tyr	Leu	L∙eu	Asn	Gln 345	Arg	Gly	Met	Fhe	Ser 350	Tyr	Thr
414 415	Gly	Leu	Ser 355	Ala	Ala	Gln	Val	Asp 360		Leu	Arg	Glu	Glu 365	Phe	Gly	Val
$\frac{418}{419}$	Tyr	Leu 370	Ile	Ala	Ser	Gly	Arg 375		Cys	Val	Pro	Gly 380	Leu	Asn	Thr	Ala
4.12 4.23	Asn 385	Val	Gln	Arg	Vāl	Ala 390	Lys	Ala	Ph⊛	Ala	Ala 395	Val	M⊖t			

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/895,041C

DATE: 06/19/2003
TIME: 10:32:24

Input Set : A:\AP09895041JUN1003.txt

Output Set: N:\CRF4\06192003\1895041C.raw